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*      20      *      40      *      60      *
exmi009 : -----HNSYQKMYEYEDALRINSNMCYPRPLAKDPONTERRTNTEEDLNCDNTOFIGDISTYSSPE : 68
cry1Aa : -----MDNNPPIHECHPYNCLSNPEVE-VLGGER-- : 28
cry1Ac : -----MDNNPPIHECHPYNCLSNPEVE-VLGGER-- : 28
cry1Ca : -----MDNNPPIHECHPYNCLSNPEVE-VLGGER-- : 27
cry1Ia : -----MKLRQODHQSFSSNA-KVDKISTDS--LKNETDIEDONINHEDCNHEEYEN--VEP-- : 53
cry3Aa1 : MIRKGGKKNPNPNSDHTDKTTE--NNEVPTNHVQYPLAETPNPTDODLNYREFLRTADNN--TEALDS-- : 67
cry3Ba : MIRKGGKKNPNPNSDHTDKTTP--NSELPTNHQYPLADNPNSTDEELNYREFLRTADNS--TEVLDS-- : 67
cry3Bb : -----MNPMPNSDHTDKTTP--NSELPTNHQYPLADNPNSTDEELNYREFLRTADSS--TEVLDS-- : 59
cry4Aa : -----HNPYQKMYEYEDASOKKLINISNMYTRPIENSFKQLLSTNYQULNNCQNNQYGGDFETFDID-- : 66
cry6Aa : -----HEIDSKITLPRHSLIHTIKLNSNRYGPGDHTNGN-- : 36
cry7Aa : -----HNLNMDGYEDSNRTLNLSNMYPTOKALSPSDQNNYQDFLSTIEREOPE--AL-- : 52
cry8Aa : -----HSPNMDGYEYEDATP--STSVSSDSNRTFANEPTDADONNMYQVLAHSGGNEPE-L-FGNPET-- : 62
cry10Aa : -----HNPYQKMYEYEDFAPNSGFSKNYSRYPLANKPHOPDNDNYQULNVCDNNQYGMNAGNFAS-- : 66
cry16Aa : -----HHYQGRNMYEDLNASNSDSNHSNMYPTPLANPQODLONNMYQULNVCEGYHIENP--FEASVR-- : 65
cry19Ba : -----HNSYQKMYEYEDAKRNTCHSNMCYPRPLANDPNYQULNTHYQULNHCCEASVAS--S-- : 59
cry24Aa : -----HNQYQKMYEYEDSSO--N-NMNPMPNRTFADDPNAVKNQGYQULNCEGSSN-- : 52
cry25Aa : -----HNPYQKMYEYEDSSO--N-NMNPMPNRTFADDPNAVKNQGYQULNCEGSSN-- : 53
cry40Aa1 : -----NSYQKMYEYEDSSS--N-NMNPMPNRTFADDPNAVKNQGYQULNCEGSSN-- : 52
n e y p n y k

*      80      *      100      *      120      *      140      *
exmi009 : AALSVRDAVLTCINSYGTISNLGVPLASQSFGLISRTIGILWAGP--DPEALNVLVEEIKKSHDQVRRENAL : 141
cry1Aa : -----IETGYTPIDISLSLTQFLSEFVPCAGFVLGLVDINQIGIFCP--SQDAPFVQDEQILNORELFARNOAH : 97
cry1Ac : -----IETGYTPIDISLSLTQFLSEFVPCAGFVLGLVDINQIGIFCP--SQDAPFVQDEQILNORELFARNOAH : 97
cry1Ca : -----ISTGSSIDISLSLTQFLSEFVPCAGFVLGLVDINQIGIFCP--SQDAPFVQDEQILNORELFARNOAH : 96
cry1Ia : -----FVSASTIQTGICGAGIGLGLVFPAGQASLSYFLGELWP--KGNQGEIPEHEWELIIOKISTYARNKAL : 125
cry3Aa1 : -----STTKDVIQKIGISVGLDGVGVFPFGGALYSFYTNFLNTHWS--EDPKAPHEQVEALNOKIADYAKKAL : 138
cry3Ba : -----STVKDAVGTGISVVGQILGVVGVFPAGALTSFYQSFNLNATPSPD--ADPKAPHAQVEVLDKQEEYAKSKAL : 139
cry3Bb : -----STVKDAVGTGISVVGQILGVVGVFPAGALTSFYQSFNLNATPSPD--ADPKAPHAQVEVLDKQEEYAKSKAL : 131
cry4Aa : -----SGELSAITIVVGTTLTGFG--FTTLGLALIGFGLTPVFFPAQDQSNLSDFTITUTKNLKKQTHASTYSNAN : 138
cry6Aa : -----FIISKQEWATGAYIQTGLGLPNEQOLRTHVNLSDISPSDFSLQYDVYCSKTSAEWUNKNLY : 102
cry7Aa : -----ASGNTAINTVYSIGATLSALGVGASFTNFYLLKAGLWPE--KGIPEDETEALNOKIADYAKKAL : 124
cry8Aa : -----FISSTIQTGICGAGIGLGLVFPAGQASLSYFLGELWP--KGNQGEIPEHEWELIIOKISTYARNKAL : 135
cry10Aa : -----SETIVGVAGLIVVGTTLTGFG--FTTLGLALIGFGLTPVFFPAQDQSNLSDFTITUTKNLKKQTHASTYSNAN : 136
cry16Aa : -----AGLGLGLGIVSTIVGFGGSIYLDITGLFYQISELWPEDDTQ--YTQDIBNHQEDLKKRTEVIRGNAL : 136
cry19Ba : -----GPSQLFKVGGSTIAKIDG--HIPEVGPLSHVNSLFWPTTEK--TVEDMKYVAMNKKOELTADTLNRT : 128
cry24Aa : -----ISPSAAITSKIVSIVKTLAKAVASS--ADSIKSLGSKITENNVSOVSHYQULNTHYQULNHCCEASVAS : 125
cry25Aa : -----SIFGTLGVLASIVISTONLATSISIGDAFALVSSGGEYWPETK--TSPLSVADNRLDREALDQNAHRT : 123
cry40Aa1 : -----AETTSIGIDLLFLMEISLGGDNTLFSINGKLIPN--HQSVSALSCHDLSTLRKEVADSVLSDAL : 118
p a

*      160      *      180      *      200      *      220      *
exmi009 : R-EDFLOGIHR--LQTRQALVYKH-----DDNRRPALTQATDNPPEKNMPKEXERN-----P21 : 198
cry1Aa : S-RUEGLSNLYQ--IAESFRELEAET-----NPALREERLQGNDSNALTATPLFAYON-----YQW : 155
cry1Ac : S-RUEGLSNLYQ--IAESFRELEAET-----NPALREERLQGNDSNALTATPLFAYON-----YQW : 155
cry1Ca : A-NUEGLSNLYQ--IAESFRELEAET-----NPALREERLQGNDSNALTATPLFAYON-----YQW : 154
cry1Ia : T-DUEGLGALA--YHDSIESVGCPR-----NTRARSVKSQIALELNVOKIPSTAVSG-----E2V : 183
cry3Aa1 : A-EDGLOQNVF--DNYVALSSOKPVSRR-----NPHSGRRELISQAESHORNSPSTFVSG-----Y2V : 199
cry3Ba : A-EDGLOQNVF--DNYVALSSOKPVSRR-----NPHSGRRELISQAESHORNSPSTFVSG-----Y2V : 200
cry3Bb : A-EDGLOQNVF--DNYVALSSOKPVSRR-----NPHSGRRELISQAESHORNSPSTFVSG-----Y2V : 192
cry4Aa : K-IDNRSNPLVS--TNNHKTLEPH-----PONTQDERTQILQHYHQNVLVNSCPPNPSCDQYNN : 204
cry6Aa : PLIKSANDIASYGRKVGCPISIKDG--YFKLQDELNDIWNSSDDAIAKAKDFKARCQ-----L2 : 165
cry7Aa : A-EDGLOQNVF--DNYVALSSOKPVSRR-----NPHSGRRELISQAESHORNSPSTFVSG-----Y2V : 182
cry8Aa : A-EDGLOQNVF--DNYVALSSOKPVSRR-----NPHSGRRELISQAESHORNSPSTFVSG-----Y2V : 193
cry10Aa : S-IYTPKQQLD--KQGEFFDKCEPART-----HANAKAHDLETTPEPIIDKQDMLKNAS-----Y2V : 197
cry16Aa : R-TADLQGVQD--DNNMKKCKDPEK-----STGNLSTVTRKTAEDSDNGAERTVNNQGPS--C2V : 197
cry19Ba : S-NISGLESIN--IYNAIAAKCKDPEK-----NIFASGELRSYINDPHILTRDQSDFLG-----C2V : 187
cry24Aa : S-SINGLVAIYHEDLGADEANMXS-----NINYQTNAAEAKTVERETFKKGIYRTSS-----S01 : 185
cry25Aa : G-KFGLQNTYNTYTKKNUODDYDTRIPANPQGSOLREARRSLEPERDPRKAGEFAEAG-----S01 : 189
cry40Aa1 : CRFDCKLKNRYEYEPYDEALRQKPLQKT--KNSDIGQVVKYELSERDNEIIGGSLARNN-----A01 : 184
g s l w f 6

*      240      *      260      *      280      *      300      *
exmi009 : LLEPVYQAANLHLHLRLDADYFC--ADQGLGDDERDNNIR-----LOGLTREYKDHLETFNOL : 257
cry1Aa : PLISVYQAANLHLHLRLDADYFC--QRGFDAATNSRYAD-----LTRLIGNYDYAVRNTITC : 214
cry1Ac : PLISVYQAANLHLHLRLDADYFC--QRGFDAATNSRYAD-----LTRLIGNYDYAVRNTITC : 214
cry1Ca : PLISVYQAANLHLHLRLDADYFC--QRGLTITNNENYAR-----LIRHIDPYADHCANTIRP : 213
cry1Ia : PLISVYQAANLHLHLRLDADYFC--KEGLSSSETSTFNR-----QVERAGDYSDHCYGHST : 242
cry3Aa1 : LPLITVYQAANLHLHLRLDADYFC--EEGYEKEDIAEFKRR-----QLKLTQCYTDHCWAEHVE : 258
cry3Ba : LPLITVYQAANLHLHLRLDADYFC--EEGYEKEDIAEFKRR-----QLKLTQCYTDHCWAEHVE : 259
cry3Bb : LPLITVYQAANLHLHLRLDADYFC--EEGYEKEDIAEFKRR-----QLKLTQCYTDHCWAEHVE : 251
cry4Aa : PLISVYQAANLHLHLRLDADYFC--KEGLSSSETSTFNR-----QVERAGDYSDHCYGHST : 242
cry6Aa : KKEAKQYDEAKMNTSLDQFEDQCKLEGVINTOKRLKEVQT-----ALNQAHCSSPAHKE : 225
cry7Aa : PLISVYQAANLHLHLRLDADYFC--QRGFDAATNSRYAD-----LTRLIGNYDYAVRNTITC : 214
cry8Aa : LLEPVYQAANLHLHLRLDADYFC--KEGLSSSETSTFNR-----QVERAGDYSDHCYGHST : 242
cry10Aa : PTLIPAYQAANLHLHLRLDADYFC--KEGLSSSETSTFNR-----QVERAGDYSDHCYGHST : 263
cry16Aa : LLEPVYQAANLHLHLRLDADYFC--KEGLSSSETSTFNR-----QVERAGDYSDHCYGHST : 257
cry19Ba : YLPSVYQAANLHLHLRLDADYFC--KEGLSSSETSTFNR-----QVERAGDYSDHCYGHST : 246
cry24Aa : TLEPTVQAANLHLHLRLDADYFC--KEGLSSSETSTFNR-----QVERAGDYSDHCYGHST : 242
cry25Aa : YLPSVYQAANLHLHLRLDADYFC--KEGLSSSETSTFNR-----QVERAGDYSDHCYGHST : 256
cry40Aa1 : LLEPVYCASCKCOLLPLDADYFC--KEGLSSSETSTFNR-----QVERAGDYSDHCYGHST : 259
l a a n h6 l d a g y y c y g

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Fig. 1A

		*	540	*	560	*	580	*	600							
axmi009	:	PANLP	SOTILSE	QKDKP	PNAGD	FSHR	SYISN	FDARRS	-SGGV	SLLTG	CAHIS	DRNR	EPK	IT	IT	534
cry1aE	:	G--	TVDSL	LVIP	PDQNS	VPRA	GF	FSHR	SHV	THS	QAAG--	AVYTL	RAP	TS	WQHR	535
cry1aC	:	G--	TVDSL	LVIP	PDQNN	VP	PRQ	GF	FSHR	SHV	THS	FRSGT	SNSV	SI	IRAP	536
cry1Ca	:	G--	TVDSL	LTLP	PDQNS	VP	PRG	GF	FSHR	SHV	THS	CHATT	VY	OR	STP	537
cry1Ia	:	G--	TVQ	LDSE	NE	LP	PE	ATG	Q	NYE	SY	SHS	SH	IC	LY	538
cry3Aa1	:	N	VGVA	SNS	IDQ	LP	PE	TTD	E	LK	GV	SHO	NY	AC	FL	539
cry3Ba	:	N	GVYL	GAQ	DS	IDQ	LP	PE	TTD	E	LK	VA	SHO	NY	AC	540
cry3Bb	:	N	HGV	VA	SNS	IDQ	LP	PE	TTD	E	LK	VA	SHO	NY	AC	541
cry4Aa	:	D	VKN	KI	FG	L	P	IL	K	R	EN	Q	NI	LP	FT	542
cry6Aa	:	T	N	H	T	S	N	O	Y	S	N	P	T	N	H	543
cry7Aa	:	N	KYD	LV	DS	IDQ	LP	PDG--	E	PI	HE	K	T	IR	CH	544
cry8Aa	:	G	QCTQ	VE	YSS	ED	L	DR	T	V	VA	E	S	Y	SH	545
cry10Aa	:	E	NNY	K	VD	DS	Y	N	I	P	K	Q	T	W	H	546
cry16Aa	:	N	KP	V	P	K	D	F	L	T	GL	E	L	A	K	547
cry19Ba	:	N	K	P	T	V	R	D	I	T	L	N	A	R	G	548
cry24Aa	:	N	K	P	Y	S	L	P	T	I	N	F	L	T	GL	549
cry25Aa	:	P	G	G	D	Y	C	G	K	Q	N	I	N	L	E	550
cry40Aa1	:	N	S	G	L	S	N	T	I	S	K	I	N	P	I	551

C

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              760              *
axmi009 : [X]ITFFNQSL-----KREQEVNLFIN : 682
cry1Aa : AEVTFEAEY-----DLERAQKAVMLFT : 628
cry1Ac : VVATLEAEY-----DLERAQKAVMLFT : 630
cry1Ca : ADATFEAES-----DLERAQKAVMLFT : 637
cry1Ia : VEVTYAEAY-----DFEKAQEKYTALET : 665
cry3Aa1 : VN----- : 652
cry3Ba : VQ----- : 659
cry3Bb : VQ----- : 652
cry4Aa : IITRSITREDREKQKLETVQQIITFYA : 702
cry6Aa : [X]----- : -
cry7Aa : [X]VVVNYAEK-----KLEKAQKAVMLFT : 658
cry8Aa : VDETFEAEQ-----DLEAAKQAVMLFT : 683
cry10Aa : ITQSVLDYTEKQMIKTKQIKVMDLV : 674
cry16Aa : TN----- : 648
cry19Ba : LGITLNQAA-----GYDTYQDNAGNTH : 659
cry24Aa : VSGSAFEYEGKQMIKTKQKAVMLFT : 673
cry25Aa : VVAFPLESEQ-----E--NKSVSYLT : 674
cry40Aa1 : VNSTALEYEGKSLKLEKQVVDVMDLV : 665

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Fig. 1C